

F. Hamed

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

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OCT 17 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540B

Source: 1643

Date Processed by STIC: 10/2/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1643

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/265,540B DATE: 10/02/2000
 TIME: 10:47:24

Input Set : A:\804Krvs2.txt
 Output Set: N:\CRF3\09292000\I265540B.raw

Does Not Comply
 Corrected Diskette Needed

OK

3 <110> APPLICANT: Parham, Christi L.
 4 Moore, Kevin W.
 5 Murgolo, Nicholas J.
 6 Bazan, J. Fernando
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 10 <130> FILE REFERENCE: DX0804
 12 <140> CURRENT APPLICATION NUMBER: US/09/265,540B
 13 <141> CURRENT FILING DATE: 1999-03-08
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1381
 21 <212> TYPE: DNA
 22 <213> ORGANISM: primate
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (132)..(1064)
 28 <220> FEATURE:
 29 <221> NAME/KEY: misc_feature
 30 <222> LOCATION: n at position 567 and 573
 31 <223> OTHER INFORMATION: n may be A, C, T, or G; translated amino acid depends on genetic code
 33 <400> SEQUENCE: 1
 34 tcgacccacg cgtccgcgct gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60
 36 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaaact 120
 38 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
 39 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
 40 1 5 10
 42 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218
 43 Ser Leu Phe Met Trp Phe Thr Tyr Ala Leu Ile Pro Cys Leu Leu Thr
 44 15 20 25
 46 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266
 47 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 48 30 35 40 45
 50 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314
 51 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 52 50 55 60
 54 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362
 55 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 56 65 70 75
 58 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410
 59 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 60 80 85 90
 62 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458
 63 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 64 95 100 105
 66 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
 67 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser

what about n's at positions 1336, 1342, 1369?
 (P.2)

RAW SEQUENCE LISTING

DATE: 10/02/2000

PATENT APPLICATION: US/09/265,540B

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set : N:\CRF3\09292000\I265540B.raw

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68 110          115          120          125
70 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
71 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
72          130          135          140
W--> 74 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602
W- 75 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
76          145          150          155
78 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
79 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
80          160          165          170
82 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
83 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
84          175          180          185
86 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
87 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
88 190          195          200          205
OK-> 90 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
OK-> 91 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
92          210          215          220
94 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
95 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
96          225          230          235
98 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
99 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
100          240          245          250
102 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
103 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
104          255          260          265
106 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
107 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
108 270          275          280          285
110 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
111 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
112          290          295          300
114 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
115 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
116          305          310
118 ggtgaagccg agaacctggt ctgcatgaca tggaaacat gaggggacaa gttgtgtttc 1144
120 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgtgttc tacaagtcta 1204
122 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
124 gwtgtgacct ctgactktg ggstkscayt tgcwtggytg agcaaccctg gaaaaagtga 1324
W--> 126 cttcatccct tgggtccaa gttttctcat ctgtaatggg ggatccctac aaaactg 1381
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 311
131 <212> TYPE: PRT
132 <213> ORGANISM: primate
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature / / / / /
135 <222> LOCATION: Xaa at residues 146, 148, 171, 214 and 225

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Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

137 <223> OTHER INFORMATION: Xaa depends on corresponding codon
 139 <400> SEQUENCE: 2
 140 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
 141 1 5 10 15
 143 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
 144 20 25 30
 146 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 147 35 40 45
 149 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 150 50 55 60
 152 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 153 65 70 75 80
 155 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 156 85 90 95
 158 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 159 100 105 110
 161 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 162 115 120 125
 164 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 165 130 135 140
 W--> 167 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 168 145 150 155 160
 W--> 170 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
 171 165 170 175
 173 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 174 180 185 190
 176 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 177 195 200 205
 W--> 179 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 180 210 215 220
 W--> 182 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 183 225 230 235 240
 185 Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe Val Trp Lys
 186 245 250 255
 188 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 189 260 265 270
 191 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 192 275 280 285
 194 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 195 290 295 300
 197 Leu Leu Arg Ala Trp Ile Ser
 198 305 310
 201 <210> SEQ ID NO: 3
 202 <211> LENGTH: 1244
 203 <212> TYPE: DNA
 204 <213> ORGANISM: primate
 206 <220> FEATURE:
 207 <221> NAME/KEY: CDS
 208 <222> LOCATION: (2)..(694)

RAW SEQUENCE LISTING

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TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

210 <400> SEQUENCE: 3

211 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49

212 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro

213 1 5 10 15

215 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97

216 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile

217 20 25 30

219 tgg gtg acg cgg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145

220 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro

221 35 40 45

223 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193

224 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa

225 50 55 60

227 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241

228 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn

229 65 70 75 80

231 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289

232 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln

233 85 90 95

235 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337

236 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly

237 100 105 110

239 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385

240 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr

241 115 120 125

243 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tgg ctg 433

244 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu

245 130 135 140

247 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481

248 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly

249 145 150 155 160

251 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529

252 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile

253 165 170 175

255 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577

256 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp

257 180 185 190

259 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625

260 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val

261 195 200 205

263 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673

264 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr

265 210 215 220

267 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724

268 Gln Asn Ser Gly Ala Val Cys

269 225 230

271 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcttccattt tctgtcccc 784

273 aaaaggcccg tcagtcctg tgaagatgta acgggtctca tgggggcgac aagcttattg 844

275 atttttttct tcaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904

RAW SEQUENCE LISTING

DATE: 10/02/2000

PATENT APPLICATION: US/09/265,540B

TIME: 10:47:24

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

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277 tatgtccccc aaagattaag atttctctta aactactaaa agacatgtaa ttatttgta 964
279 gcaaatgggc gtctggcagc cctctgacac ttttctgta gcagccagga cagcaggtcc 1024
281 cctccttgat gaagcccttc gggcagacca tgtcacctgt ccagcctgc cccaagaagg 1084
283 gacattaagt ggccttctt catatccaaa cactgggtt gaaatgtgat tagccttgta 1144
285 aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204
287 aactttttta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244
290 <210> SEQ ID NO: 4
291 <211> LENGTH: 231
292 <212> TYPE: PRT
293 <213> ORGANISM: primate
295 <220> FEATURE:
296 <221> NAME/KEY: misc_feature
297 <222> LOCATION: Xaa at residue 64
298 <223> OTHER INFORMATION: Xaa translated amino acid depends on corresponding codon
300 <400> SEQUENCE: 4
301 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
302 1 5 10 15
304 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
305 20 25 30
307 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
308 35 40 45
310 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
311 50 55 60
313 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
314 65 70 75 80
316 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
317 85 90 95
319 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
320 100 105 110
322 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
323 115 120 125
325 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
326 130 135 140
328 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
329 145 150 155 160
331 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
332 165 170 175
334 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
335 180 185 190
337 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
338 195 200 205
340 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
341 210 215 220
343 Gln Asn Ser Gly Ala Val Cys
344 225 230
347 <210> SEQ ID NO: 5
348 <211> LENGTH: 337
349 <212> TYPE: PRT
350 <213> ORGANISM: primate

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VERIFICATION SUMMARY

DATE: 10/02/2000

PATENT APPLICATION: US/09/265,540B

TIME: 10:47:25

Input Set : A:\804Krvs2.txt

Output Set: N:\CRF3\09292000\I265540B.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:224 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:224 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821.825. Applicant's attention is directed to these regulations, published at 114 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

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